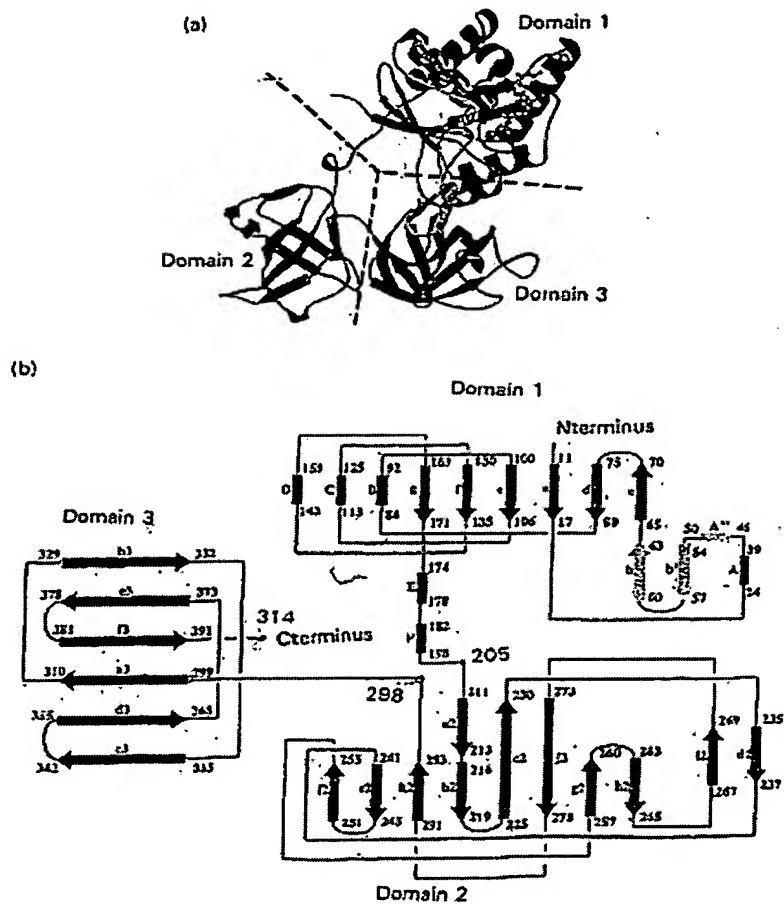


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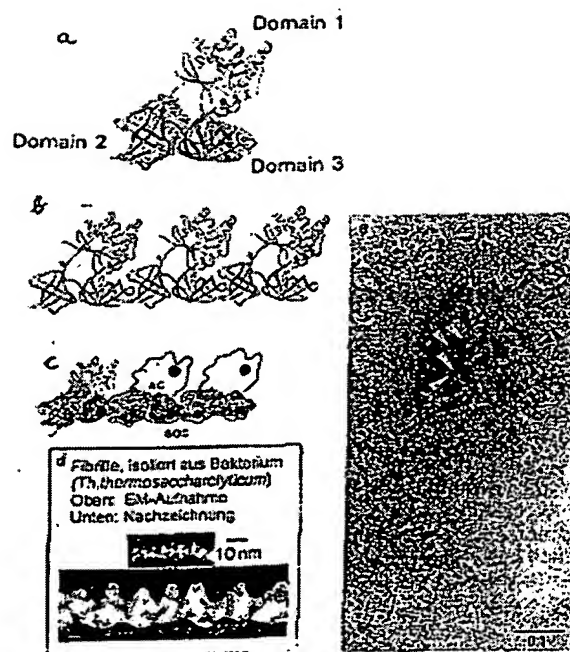
Figur 1



[Key to Figure 1:]

Figur = Figure

Figur 2



[Key to Figure 2:]

Figur = Figure

Fibrille, isoliert aus Bakterium = Fibrilla, isolated from the bacterium

Oben: EM-Aufnahme = Above: EM image

Unten: Nachzeichnung = Below: Copy

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Fig. 3

(a1)

Vektor pEGFP (Clontech):

```

      BsrGI      STOP      EcoRI
GAC GAG CTG TAC AAG TAA AGC GGC CGC GAC TCT AGA ATT CCA
CTG CTC GAC ATG TTC ATT TCG CCG GCG CTG AGA TCT TAA GGT

```

BsrGI-Schnittstelle:

```

T  GTACA
ACATG T

```

EcoRI-Schnittstelle:

```

G  AATTC
CTTAA G

```

Synthetisch hergestelltes Oligonukleotid zur Einklonierung des His-Tags in den Vektor:

```

5' BsrGI      BsrGI      EcoRI 3'
G TAC AAG CTT CAT CAC CAT CAC CAT CAC TAA CTG TAC AAG TAAG
      TTC GAA GTA GTG GTA GTG GTA GTG ATT GAC ATG TTC ATTCTTAA
3'                                     5'
Tyr-Lys-Leu-His-His-His-His-His-His-STOP-

```

Ergebnis: pEGFP(His)

(a2)

Vektor pEGFP(His):

```

GCC TGC AGG -t- ACC ATG GTG
CGG ACG TCC -t- TGG TAC CAC

```

PstI-Schnittstelle:

```

CTGCA G
G  ACGTC

```

NcoI-Schnittstelle:

```

C  CATGG
GGTAC C

```

Fusionsstellen zum EF-Tu-Gen:

```

      Start EF-Tu      Start EGFP
5' PstI      HindIII  NcoI 3'
ACT AGC TGC AGC ATG TCT AAA -t- CTG GGC AAG CTT ACC ATG GTG
TGA TCG ACG TCG TAC AGA TTT -t- GAC CCG TTC GAA TGG TAC CAC
3'                                     5'
Thr-Ser-Cys-Ser-Met-Ser-Lys-----Leu-Gly-Lys-Leu- Thr-Met-Val

```

[Key to Figure 3:]

Vektor = Vector

Schnittstelle = Interface

Synthetisch hergestelltes Oligonukleotid zur Einklonierung des His-Tags in den Vektor =

Synthetically produced oligonucleotide for cloning the His tag in the vector

Ergebnis = Result

Fusionsstellen zum EF-Tu-Gen = Fusion points in the EF-Tu gene

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(a3)

Fusionsstellen zur Domäne 3:

```

5'      PstI      Cys HindIII      NotI      3'
ACT AGC TGC AGC GCT AAG CCG -3- CTC GGC TGC AAG CTT ACC ATG GTG
TGA TCG ACG TCG CGA TTC GGC -3- GAC CCG ACG TTC GAA TGG TAC CAC
3'
Thr-Ser-Cys-Ser-Ala-Lys-Pro-----Leu-Gly-Cys-Lys-Leu-Thr-Met-Val

```

[Key to 4/15:]

Fusionsstellen zum Domäne 3 = Fusion points in domain 3

UTGTTGAGCA AAGGCGAGGA GCTGTTCCAC GGGTGGTGC CCATCCTGGT CGAGCTGGAC GGGGAGTAA ACGGCCACAA

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CTTACGCTG TCCGGGAGG GCGAGGGGA TCCACCTAC GGCACCTGA CCGTCAAGT CATCTGACC ACCGGCAGC
TCCCGTGCC CTGGCCACC CTCTGACCA CCGGTGACG TCGTTCAGC GCTACCCCGA CCACATGAG
CAGCAGACT TCTTCAGTC CCGCATGCC GAAGCTACG TCCAGAGCG CACCATCTTC TTCAGGAGC AGGCGACTA
CAGACCCGC CCGAGGTGA AGTTGGAGG CCGACCTTC GTGACCGCA TCGAGCTGA GGGCATGAC TTCNAGGAGG
ACGCGACAT CCTGGGGAC AGCTGAGT ACACCTACA CAGCCACAC GTCTATATCA TGGCCGACAA CCGAGAGAC
GCGATCAGG TCACTTCAA GATCGGCAC ACATCGAGG AGGCTGCG CCGACTGCG CCGACTACG AGCGAACAC
CCCATCGC GCGGCCCG TGTGCTGCC CCGACGAC TACTGAGCA CCGAGTCCG CCGTACCAA GACCCGACG
ACACCCCGA TCACTGCTC CTGCTGAGT TGTGACCG CCGCGGNTC ACTCTGCGA TCGCAGAGG TGTGACG

HLs-Tag:

CTTCATCAC ATCAACATCA CTAACTGTAC AAGTACGAGG

pEGFP-Vektor:

CAACTGAGC CCGTGGCTA CCAATACCA CTGCTGCT GTCAAAATA ATAGGCTAC TAGTGGCG TAGGGCCCT
TTGCTGCG CCGTTGCT GATGACGCT AATCTCTG ACATGTCG CTCCGAGA CGGTACAGC TTCTCTGTA
GGGATGCG GAGGAGACA AGCGCTGAG CCGGTGTCG GGTGCTGA ACTATGCGC
ATCAGAGAG ATTCTACTA GACTGCACA TATCGCTGT GAATACCG ACAGTGGT AGGAGAAA TCCGCTCA
GGCGGCTTA AGGCTCTT GATGCTCTA TTTTATAG TTAATGTCAT GATATATAG GTTCTTAGA CGTGAGTGG
CACTTTTCG GGAATGTC GCGAACCC TATTTGTTA TTTTCTAAA TACATCABA TATGATCCG CTCATGAGC
ATAACCTTG ATATGCTT CATATATTT GAAAGGAAA GAGT



CCCTCCCGTA TCGTAGTTAT CTACAGACG GGGGTGACG CAATATGCA TGAACAAAT AGACAGATCG CTGAGATAGG

[Key to 6/15:]

Vektor = Vector

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TGCCTCACTG ATTACGATT GGTACCTGTC AGACCAAGTT TACTCATATA TACTTAGAT TCATTATATA CTCCTTTT
 AATTAAAG GATCTAGGTG AGATCCTTT TTGATAATCT CAGACCAAA ATCCCTTAC GTRGTTC GTCCACTGA
 GGTCCAGACC CC
 [REDACTED]
 GGCC TTTCCTGGC CTTTGTCTCA CAGTCTCTT CCTGCTTAT CCCTGATTC TGTGGATAC
 CGTATTACCG CTTTCAGTG AGCTGATACC GCTCCGCGA GCGGACGAC CGAGCCGAGC GATCTAGTGA GCGAGGAGC
 CGAAG

Sequenz 2 Lac-Promotor

Sequenz 3 Lac-Operator

Sequenz 4 Ribosomen-Bindungsstelle

Sequenz 5 Ampicillin-Resistenz-Gen

Sequenz 6 pUC Plasmid-Replikations-Origin

1. NotI
 2. PstI
 3. NcoI
 4. BspGI
 5. EcoRI

[Key to 7/15:]

Sequenz: Lac-Promotor = Sequence: Lac-promoter

Ribosomen-Bindungsstelle = Ribosome binding site

Ampicillin-Resistenz-Gen = Ampicillin resistance gene

Klonierungsstellen = Cloning sites

The sequence contains four silent mutations () that are clearly present according to sequence analysis:

(1) To be: TAT, Is: TA -> Tyr; codon usage (entire E. coli genome) is changed from 16.2 to 12.2

(2) To be: TAC, Is: TA -> Tyr; codon usage (entire E. coli genome) is changed from 12.2 to 16.2

(3) To be: GCA, Is: GC -> Ala; codon usage (entire E. coli genome) is changed from 20.1 to 33.6

(4) To be: ATT, Is: AT -> Ile; codon usage (entire E. coli genome) is changed from 30.3 to 25.1 (frequency per thousand)

Sequenz des Konstrukts Domäne 3 von EF-Tu-GFP-His im Vektor pEGFP (Clontech) (SEQ ID NO:2)
(b2)

pEGFP-Vektor:

AGGCCCAAT AGCAAACG CCTCTCCG CGGTGGC GATTATTA TGAGCTGC ACGACAGTT TCCGACTGG
AAGCGGGCA
CATCGTGGAC

Domäne 3 von EF-Tu:

GCTAAGCGG GCACCATCAA GCGGCACCC AGGTTGAGT CTGAAGTGA CATCTGTCC AAGATGAAG GCGCGGTCA
TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC CGTACTACTG ACGTGACTGG TACCATGAA CTGCGGGAAG
GCGTAGAGAT GGTAAATGCG GCGCAGACACA TCHAAATGGT TGTACCCCTG ATCCACCCGA TCGCGATGA CGACGTCTG
CGTTTCGCA TCCGTGAAG GCGCGGTACC GTTGGCGCGG GCGTTGTAGC TAAGTTCTG GGTGC

Prüfung-Vektor:

AGCTAGE

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[illegible]

Wiss-Tag:

CTTCATCACC ATCACCATCA CTAACTGTAC AAGTACGCTTGG

[Key to 9/15:]

Sequenz des Konstrukts Domäne 3 von EF-Tu-GFP-His im Vektor pEGFP (Clontech) (SEQ ID

No: 2) (b2) = Sequence of the domain-3 construct of EF-Tu-GFP-His in the vector

pEGFP (Clontech) (SEQ ID No: 2) (b2)

Vektor = Vector

Domäne = Domain

pEGFP-Vektor:

CAACTGAGCG CCGGTCCGTA CCATTACCAA CTTGTCTGGT GTCAAAATA ATAGCCTAC TAGTCGGCG TACGGGCCCT
TTCTCTCCG GCGTTTCGGT GATGACGGTG AAACCTCTG ACACATCCAG CTCCTGGAGA CGGTACAGC TTGTCTGTAA
GCGATGCCG GGAGCAGCA AGCCGTCAG GCGGTCAG CCGGTGTCG GGTGGCTTA ACTATCCGC
ATCAGAGCG ATTGTACTGA GAGTGCACCA TATGGGTGT GAATACCGC ACAGATCCGT AAGGAGAAA TACCGCATCA
GGCGCCCTTA AGGCCTCGT GATACGCCA TTTTATAGG TTAATGTCAT GATAATATG GTTCTTAGA CGTCAGGTGG
CACTTTTCGG GGAATGTC GCGGAACCC TATTTGTTA TTTTCTAA TACATCAA TATGTATCCG CTCATGAGAC
AATACCTG AATAATGCTT CAATATATT GAAAGGAA GAGT

CCCTCCGTA TCGTAGTAT CTACACGACG GGGAGTCAGG CAACATATGA TGAACGAAT AGACAGATCG CTGAGATAGG
TGCTCACTG ATTAGCATT GGTAACTGC AGACCAAGTT TACTCATTA TACTTTAGAT TGATTAATA CTTCATTTT
AATTAAG GATCTAGGTG AGATCCTTT TTGATATCT CATGACCATA ATCCCTTAC GTGAGTTTC GTTCCACTGA
GGTCAGACC CC

[Key to 10/15:]

Vektor = Vector

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GGCC TTTTGCTGGC CTTTGTCTCA CATGTTCTTT CCTGGCTTAT CCCCTGATTC TGTGGATAC
CGATTACCG CCTTGAGTG AGCTGATACC GCTCGGCCCA GCGAGGACG CAGTCAGTGA CCGAGGAGC
GGAC

Sequenz Lac-Promotor

Sequenz Lac-Operator

Sequenz Ribosomen-Bindungsstelle

Sequenz Ampicillin-Resistenz-Gen

Sequenz pUC Plasmid-Replikations-Origin

Sequenz 5. GGTAC PstI
6. GATC NcoI
7. TGA BspCI
8. GATC EcoRI

Die Sequenz enthält eine silent mutation (ATG -> ATT), die laut Sequenzanalyse eindeutig vorhanden ist:

Soll: ATT, Ist: ATG -> Ile; Codon usage (gesamtes Genom E. coli) ändert sich von 30,3 zu 25,1 (Frequenz pro Tausend)

[Key to 11/15:]

Sequenz: Lac-Promotor = Sequence: Lac-promoter

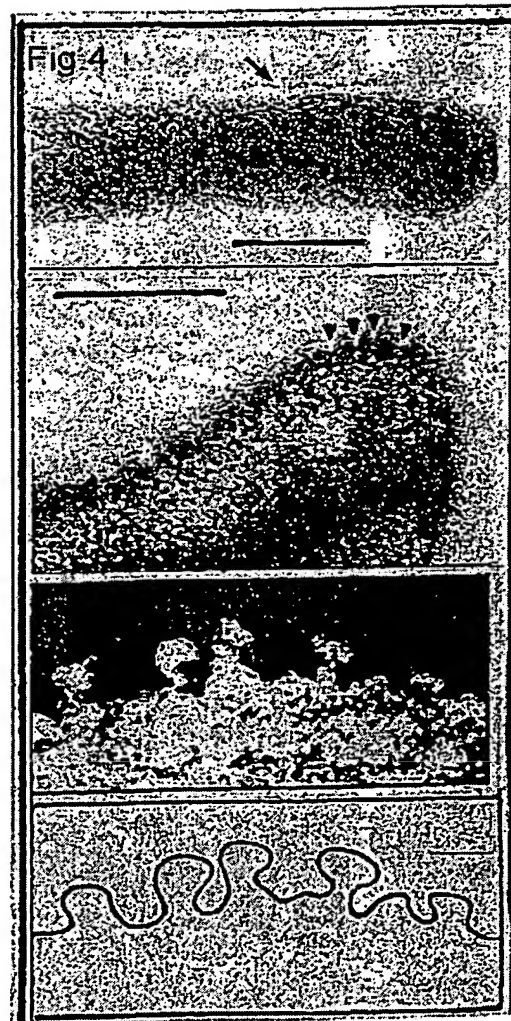
Ribosomen-Bindungsstelle = Ribosome binding site

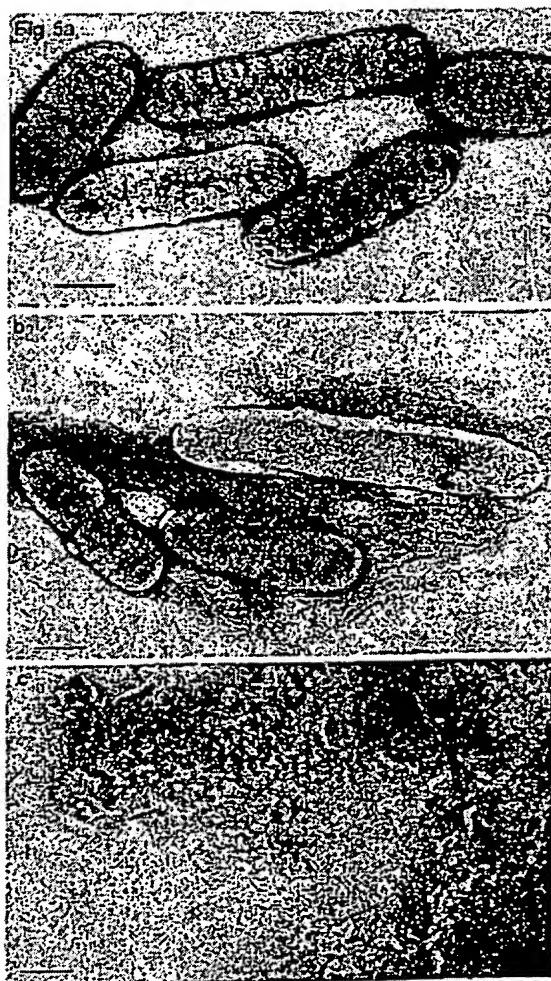
Ampicillin-Resistenz-Gen = Ampicillin resistance gene

Klonierungsstellen = Cloning Sites

[last sentence:] The sequence contains a silent mutation (), which is clearly present according to the sequence analysis:

To be: ATT, Is: AT -> Ile; codon usage (entire E. coli genome) is changed from 30.3 to 25.1 (frequency per thousand)





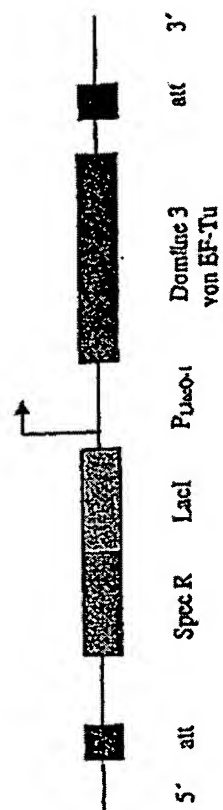
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Figur 7



[Key to Figure 7:]

Figur = Figure

Domäne 3 von EF-Tu = Domain 3 of EF-Tu

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